AMENDMENTS TO THE CLAIMS WITH MARKINGS TO SHOW CHANGES MADE, AND LISTING OF ALL CLAIMS WITH PROPER IDENTIFIERS

1. (Currently amended) A method for determining a target nucleic acid sequence, the method comprising the steps of:

(a) contacting a preparation comprising the target nucleic acid sequence and a non-target nucleic acid sequence, the target nucleic acid sequence and the non-target nucleic acid sequence each having a first region of common sequence upstream of a first region of dissimilar sequence upstream of a second region of dissimilar sequence, - with an oligonucleotide primer complementary to at least a portion of the first region of common sequence, under conditions to hybridize the primer thereto; and

(b) subjecting the resulting preparation to a sequencing reaction, such that the sequencing reaction proceeds into the second region of dissimilar sequence of the target nucleic acid sequence, thereby determining at least the second region of dissimilar sequence of the target nucleic acid sequence; and wherein the method further comprises a step of blocking the sequencing reaction between the primer and the non-target nucleic acid sequence, such that the sequencing reaction does not proceed into the second region of dissimilar sequence of the non-target nucleic acid sequence, wherein the blocking step comprises contacting the preparation with a terminator nucleotide, under conditions to incorporate the terminator nucleotide into the extended or unextended primer hybridized to the non-target nucleic acid sequence but not into the extended or unextended primer hybridized to the target nucleic acid sequence.

2. (Previously presented) The method according to claim 1, wherein the target nucleic acid sequence and the non-target nucleic acid sequence each have a second region of common sequence which lies between the first and second regions of dissimilar sequence.

3. (Cancelled)

4. (Previously presented) The method according to claim 3, wherein the conditions are such that the terminator nucleotide is incorporated into substantially all of the extended or unextended primer hybridised to the non-target nucleic acid sequence, before the sequencing reaction reaches the second region of dissimilar sequence.

5. (Previously presented) The method according to claim 4, wherein contacting the preparation with the terminator nucleotide is after step (a) and before step (b) of claim 1.

6. (Previously presented) The method according to claim 4, wherein the terminator nucleotide is complementary to a first nucleotide comprised in the first region of dissimilar sequence of the non-target nucleic acid sequence, but the terminator nucleotide is not complementary to a second nucleotide at a corresponding position in the target nucleic acid sequence.

7. (Previously presented) The method according to claim 3, wherein the terminator nucleotide is a dideoxy nucleotide.

8. (Previously presented) The method according to claim 7, wherein the terminator nucleotide is capable of covalently cross-linking the primer to the non-target nucleic acid.

9. (Previously presented) The method according claim 1, wherein the second region of dissimilar sequence comprises a single nucleotide.

10. (Previously presented) The method according to ~~any preceding~~ claim 1, wherein the first region of dissimilar sequence comprises a single nucleotide.

11. (Previously presented) The method according to ~~any preceding~~ claim 1, wherein the sequencing reaction comprises a method of sequencing based on detection of released pyrophosphate.

12. (Previously presented) The method according to claim 11, wherein the sequencing reaction comprises pyrosequencing.

13. (Previously presented) The method according to claim 1, wherein said preparation comprises DNA derived from two or more subjects.

14. (Currently amended) A method for determining a plurality of target nucleic acid sequences which method comprises the steps of:

(a) contacting a preparation, wherein the plurality of target nucleic acid sequences is comprised in a preparation comprising a plurality of target nucleic acid sequences and a plurality of corresponding non-target nucleic acid sequences, wherein each target nucleic acid sequence in the preparation corresponds to one or more corresponding non-target nucleic acid sequences in the preparation, each target nucleic acid sequence and each corresponding non-target nucleic acid sequence has a first region of common sequence upstream of a first region of dissimilar sequence upstream of a second region of dissimilar sequence, the first region of common sequence of each target nucleic acid sequence is the same as the first region of common sequence of its corresponding non-target nucleic acid sequences, the first region of dissimilar sequence of each target nucleic acid sequence is different to the first region of dissimilar sequence of its corresponding non-target nucleic acid sequences, the second region of

dissimilar sequence of each target nucleic acid sequence is different to the second region of dissimilar sequence of its corresponding non-target nucleic acid sequences, - with a plurality of oligonucleotide primers, wherein each primer is complementary to at least a portion of the first region of common sequence of a target nucleic acid sequence and its corresponding non-target nucleic acid sequence, under conditions to hybridize the primer thereto; and

(b) subjecting the resulting preparation to a sequencing reaction, such that the sequencing reaction proceeds into the second region of dissimilar sequence of the target nucleic acid sequences, thereby determining at least the second region of dissimilar sequence of each target nucleic acid sequence;and wherein the method further comprises a step of blocking the sequencing reaction between each primer and each corresponding non-target nucleic acid sequence, such that the sequencing reaction does not proceed into the second region of dissimilar sequence of each corresponding non-target nucleic acid sequence, wherein the blocking step comprises contacting the preparation with a terminator nucleotide, under conditions to incorporate the terminator nucleotide into the extended or unextended primer hybridized to the non-target nucleic acid sequence but not into the extended or unextended primer hybridized to the target nucleic acid sequence.

15. (Previously presented) The method according to claim 1, wherein the target nucleic acid sequence and the non-target nucleic acid sequence comprise one or more further regions of dissimilar sequence downstream of the second region of dissimilar sequence.

16. (Previously presented) The method for determining the haplotype of a subject from a sample comprising DNA from the subject, comprising a method as defined in claim 1, wherein the preparation comprises the

sample, the target nucleic acid sequence includes a locus on a first chromosome of a pair of chromosomes, the non-target nucleic acid sequence comprises the corresponding locus on the second chromosome of the pair, the locus comprising two or more single nucleotide polymorphisms for which the subject is heterozygous, wherein the sequencing reaction is conducted to determine the sequence of the locus on the first chromosome of the pair thereby determining the haplotype of the subject.

17. (Previously presented) The method according to claim 16, wherein the locus comprises a human Class I or Class II HLA gene.

18. (Currently amended) A method of pyrosequencing a sample of DNA from a subject for determining the haplotype of a the subject comprising the steps of: pyrosequencing a target locus on a first chromosome of a pair, the target locus comprising two or more single nucleotide polymorphisms, and blocking from sequencing the corresponding locus on the second chromosome of the pair by incorporation of a terminator nucleotide into an oligonucleotide primer hybridized to the second chromosome.

19-23. (Cancelled)